



```

Db      1 MSKGEELFTGVPIVLVELDGVNGHKFSVSGSGSDATYGKLTFLCTCTGKLPVPMPTL 60
OY      62 VTTLSYGVQCFSRYPDMKQHDFFKSAMPGYGVQERTIFFKDDGNTKTAEVKFFGDTLV 121
Db      61 VTTGTVGVQCFSRYPDMKQHDFFKSAMPGYGVQERTIFFKDDGNTKTAEVKFFGDTLV 120
OY      122 NRIELAGIDKEDGNILGHKLENYNSHNYIMADKQNGIKYKFKIRHNIEDGSVOLAD 181
Db      121 NRIELAGIDKEDGNILGHKLENYNSHNYIMADKQNGIKYKFKIRHNIEDGSVOLAD 180
OY      182 HYQONTPTGCGPVLPPDNHLYSTQSALSKDQPKNEKRDHNVLLGFTVTAAGITLGMDEL 239
Db      181 HYQONTPTGCGPVLPPDNHLYSTQSALSKDQPKNEKRDHNVLLGFTVTAAGITLGMDEL 238

RESULT 2
OY 027903 37503 PRELIMINARY; PRT; 238 AA.
AC Q27903
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Green fluorescent protein.
OS GFP identified.
OC unclassified.
NCBI_TaxID=32644;
RN [1]
RP Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RX MEDLINE=9729982; PubMed=9154981;
RT "Enhanced expression in tobacco of the gene encoding green fluorescent protein by modification of its codon usage."
RL Plant Mol. Biol. 33:989-999(1997).
DR EMBL; X96418; CAA65278.1;
DR HSP; P42212; IGFL;
DR PFI; PF01353; GFP.1;
DR PFI; PF01353; GFP.2;
DR PRINTS; PR01229; GFPLORESCENT.
DR PRODOM; PD013756; Green_fl_protein; 1.
DR PROSITE; PS00294; PRENLTATION; UNKNOWN_1.
SQ SEQUENCE 238 AA: 26884 MW: CA932D47262AD3 CRC64;
Query Match 97.3%; Score 1239; DB 5; Length 238;
Best Local Similarity 97.5%; Pred. No. 1,56-94;
Matches 232; Conservative; PRT; 238 AA;
OY 2 VSKGEELFTGVPIVLVELDGVNGHKFSVSGSGSDATYGKLTFLCTCTGKLPVPMPTL 61
Db 1 MSKGEELFTGVPIVLVELDGVNGHKFSVSGSGSDATYGKLTFLCTCTGKLPVPMPTL 60
OY 62 VTTLSYGVQCFSRYPDMKQHDFFKSAMPGYGVQERTIFFKDDGNTKTAEVKFFGDTLV 121
Db 61 VTTGTVGVQCFSRYPDMKQHDFFKSAMPGYGVQERTIFFKDDGNTKTAEVKFFGDTLV 120
OY 122 NRIELAGIDKEDGNILGHKLENYNSHNYIMADKQNGIKYKFKIRHNIEDGSVOLAD 181
Db 121 NRIELAGIDKEDGNILGHKLENYNSHNYIMADKQNGIKYKFKIRHNIEDGSVOLAD 180
OY 182 HYQONTPTGCGPVLPPDNHLYSTQSALSKDQPKNEKRDHNVLLGFTVTAAGITLGMDEL 239
Db 181 HYQONTPTGCGPVLPPDNHLYSTQSALSKDQPKNEKRDHNVLLGFTVTAAGITLGMDEL 238

RESULT 3
OY 096701 PRELIMINARY; PRT; 758 AA.
AC Q96701
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Raichu404X.
GN RAICHU404X.

Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
(1)
SEQUENCE FROM N.A.
MEDLINE=9111065-1068(2001);
MEDLINE=91122811; PubMed=11429608;
MOCHIZUKI N., Yamashita S., Kurakawa K., Ohba Y., Nagai T.,
MIYAWAKI A., Matsuda M.;
"Spacio-temporal images of Growth Factor-induced Activation of Ras and
Rapl-1."; 11:1065-1068(2001);
EMBL; AB051846; BAB61868.1;
InterPro; IPRO00786; Green_fl_protein.
InterPro; IPRO01230; Prenyl_site.
InterPro; IPRO01806; Ras_trnsfmg.
InterPro; IPRO03116; RBD.
Pfam; PF00002; Ras.
Pfam; PF01353; GFP.1.
Pfam; PF00071; ras; 1.
Pfam; PF02196; RBD; 1.
PRODOM; PD013756; Green_fl_protein; 2.
TIGRFAMs; TIGR00231; smallGTP; 1.
PROSITE; PS00294; PRENLTATION; UNKNOWN_1.
SQ SEQUENCE 758 AA: 85015 MW: 8612408F607CFD49 CRC64;
Query Match 96.3%; Score 1227; DB 4; Length 758;
Best Local Similarity 97.5%; Pred. No. 6,9e-93;
Matches 231; Conservative; 2; Mismatches; 4; Indels; 0; Gaps; 0;
OY 1 MYSKGEELFTGVPIVLVELDGVNGHKFSVSGSGSDATYGKLTFLCTCTGKLPVPMPT 60
Db 498 MYSKGEELFTGVPIVLVELDGVNGHKFSVSGSGSDATYGKLTFLCTCTGKLPVPMPT 557
OY 61 LVTLSYGVQCFSRYPDMKQHDFFKSAMPGYGVQERTIFFKDDGNTKTAEVKFFGDTLV 120
Db 558 LVTLSYGVQCFSRYPDMKQHDFFKSAMPGYGVQERTIFFKDDGNTKTAEVKFFGDTLV 617
OY 121 VNRLEAGIDKEDGNILGHKLENYNSHNYIMADKQNGIKYKFKIRHNIEDGSVOLAD 180
Db 618 VNRLEAGIDKEDGNILGHKLENYNSHNYIMADKQNGIKYKFKIRHNIEDGSVOLAD 677
OY 181 DRYQONTPTGCGPVLPPDNHLYSTQSALSKDQPKNEKRDHNVLLGFTVTAAGITLGMDEL 237
Db 678 DRYQONTPTGCGPVLPPDNHLYSTQSALSKDQPKNEKRDHNVLLGFTVTAAGITLGMDEL 734

RESULT 4
OY 017105 PRELIMINARY; PRT; 238 AA.
AC Q17105
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE GFP fluorescent protein (fragment).
OS Aequorea victoria (Jellyfish).
OC Aequorea victoria; Metazoa; Cnidaria; Hydrozoa; Hydroids; Leptomedusae;
OC Aequoreidae; Aequorea.
NCBI_TaxID=6100;
SEQUENCE FROM N.A.
WATKINS J.N., Campbell A.K.;
Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
EMBL; X83959; CAA58789.1;
HSP; P42212; IGFL.
InterPro; IPRO00086; Green_fl_protein.
InterPro; IPRO01353; GFP.1.
PRINTS; PR01229; GFPLORESCENT.
PRODOM; PD013756; Green_fl_protein; 1.
NON_TER 238
PT

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Q8WTC6: 01-MAR-2002 (TrEMBLrel. 20, Created)  
AC 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 21, Last annotation update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Green fluorescent protein.  
DE [Protein Data Bank](#)  
OS [Aequorea victoria](#)  
OC [Aequorea macrocytella](#)  
OC [Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydrozoa; Leptomedusae;](#)  
OC [Aequoreidae; Aequorea](#).  
OX NCBI\_Taxid=147615;  
[1]  
SEQUENCE FROM N.A.  
RP STRAIN=GFPM30V;  
RP [Luo X., Xia N.S., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.](#)  
RP ["Colorful mutants of green fluorescent protein from Aequorea macrocytella.";](#)  
RT Submitted (Oct-2001) to the EMBL/GenBank/DDBJ databases.  
RL EMBL: AF435431; AML33916.1;  
RL InterPro: IPR000786; Green.fl.protein.  
RL Pfam: PF013756; GFP.G1.  
RL Pfam: PF013756; Green.fl.protein.1.  
SD [SEQUENCE 238 AA; 27015 MW; 688FD75E88926903 CRC64;](#)

	Query Match	95.2%	Score 1085;	DB 5;	Length 238;
	Best Local Similarity	82.4%;	Pred. M. 7.9e-82;		
	Matches 196;	Conservative 20;	Mismatches 22;	Indels 0;	Gaps 0;
QY	2	VSGELPFGVPIVLKDYGDVNGHFGVSGECEDATYGALFLAICTTGKLPVMPPTL	61		
DB	1	MSGELPFGVPIVLKDYGDVNGHFGVSGECEDATYGKLEIFICTTGKLPVMPPTL	60		
QY	62	VTTLGVQCFSRYPDHMKHDFKSGAPGVTVQERTIFFKDDGNTKRAEVKFGDVLW	121		
DB	61	VTTLGVQCFSPYDPMKMDGFGSGAPGVTVQERTIFFKDDGNTKRAEVKFGDVLW	120		
QY	122	NTELGLGDFEDNTGLKLEVNTSNPTIMADKQRIKVFKEIHNHEDGSLVOLAD	181		
DB	121	NRELKGNDFEDNTGLKLEVNFSHNVTIMPKANGIKVFKEIHNHEDGGVOLAD	180		
QY	182	HYQQNTPIGDGVPLLPDHNTLSQSLASDPSKPKRDHMLGPFVTAAGTILGNELYK	239		
DB	181	HQYNVLGGDGPVLLPDHNTLSQSLASDPSKPKRDHMLGPFVTAAGTILGNELYK	238		

QW695;	01-MAR-2002 (TREMBLrel. 20, Created)
AC	01-MAR-2002 (TREMBLrel. 20, Created)
AD	01-MAR-2002 (TREMBLrel. 20, Created)
AE	01-MAR-2002 (TREMBLrel. 21, Last annotation update)
AF	Green fluorescent protein.
AG	GN
AN	GPXM
AO	Asqueura macrodactyla.
AP	OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Leptomedusae;
AQ	OC Asqueuridae; Asqueura.
AR	NCBI_TaxId=147615;
AS	OC
AT	RNA
AV	[1]
AW	SEQUENCE FROM N.A.
AX	RP STRAIN=GPXM, AND GPFDAHX;
AY	RP
AZ	RP
BA	Luo W.X., Zhang J., Fang H.J., Xie X.Y., Li S.W., Qin Y.X., Fang S.Q.,
BB	Li S.J., Xia N.S.;
BC	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
BD	NCBI_TaxId=147615;
BE	OC EMBL; NCBI321; AK02063.1;
BF	OC EMBL; NCBI321; AK02059.1;
BG	InterPro: IPR000786; Green_fl_protein.
BH	PFam: PF01353; GFP; 1.
BI	DR
BJ	DR
BK	DR
BL	DR
BM	DR
BN	DR
BO	DR
BP	DR
BQ	DR
BR	DR
BS	DR
BT	DR
BV	DR
BW	DR
BX	DR
BY	DR
BZ	DR
CA	DR
CB	DR
CC	DR
CD	DR
CE	DR
CF	DR
CG	DR
CH	DR
CI	DR
CJ	DR
CK	DR
CL	DR
CM	DR
CN	DR
CO	DR
CP	DR
CQ	DR
CR	DR
CS	DR
CT	DR
CU	DR
CV	DR
CW	DR
CX	DR
CY	DR
CA	DR
CB	DR
CC	DR
CD	DR
CE	DR
CF	DR
CG	DR
CH	DR
CI	DR
CJ	DR
CK	DR
CL	DR
CM	DR
CN	DR
CO	DR
CP	DR
CQ	DR
CR	DR
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CT	DR
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CY	DR
CA	DR
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CC	DR
CD	DR
CE	DR
CF	DR
CG	DR
CH	DR
CI	DR
CJ	DR
CK	DR
CL	DR
CM	DR
CN	DR
CO	DR
CP	DR
CQ	DR
CR	DR
CS	DR
CT	DR
CU	DR
CV	DR
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CX	DR
CY	DR
CA	DR
CB	DR
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CE	DR
CF	DR
CG	DR
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CI	DR
CJ	DR
CK	DR
CL	DR
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CB	DR
CC	DR
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CJ	DR
CK	DR
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CQ	DR
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CU	DR
CV	DR
CW	DR
CX	DR
CY	DR
CA	DR
CB	DR
CC	DR
CD	DR
CE	DR
CF	DR
CG	DR
CH	DR
CI	DR
CJ	DR
CK	DR
CL	DR
CM	DR
CN	

Query Match	84.9%;	Score 1081;	DB 5;	Length 238;
Best Local Similarity	81.9%;	Pred. No. 1.7e-81;		



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QY 2 VSKGEELFTGVPLVLELDGVNKHKFSVSGEGDGYATYKGLTKLFCTCTCKLPVWPPTL 61
DB 1 VSKGEELFTGVPLVLELDGVNKHKFSVSGEGDGYATYKGLTKLFCTCTCKLPVWPPTL 60
QY 62 VTTLSGVQCFSPYDPMKHQDFPKSAMPEGYQVQERTIFFKDDGNYKTRAEVKEGDTLV 121
DB 61 VTTLSGVQCFSPYDPMKHQDFPKSAMPEGYQVQERTIFFKDDGNYKTRAEVKEGDTLV 120
QY 122 NRTELKGFDEKNGHLKLEYNFNSHNYIMADKQKNGIKVNFKIRHNIDSGVOLAD 181
DB 121 NRTELKGFDEKNGHLKLEYNFNSHNYIMADKQKNGIKVNFKIRHNIDSGVOLAD 180
QY 182 HYQNTPTIGDGPVLPDNYLSQTASLKDQPKRDNHVLGFTVTAAGITLGMDELK 239
DB 181 HYQNTNPLDGPVLPINHYLSQTASLKDQPKRDNHVLGFTVTAAGITLGMDELK 238
RESULT 11
QY Q8WTC7 PRELIMINARY; PRT; 238 AA.
AC Q8WTC5;
DB DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE The green fluorescent protein.
GN GFP.
OC Aequorea macrodactyla.
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroids; Leptomedusae;
OC Aequoreidae; Aequorea.
OX NCBI_TaxID=147615;
RN RP
RC STRAIN=GFXM163;
RA Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.,
RA Li S.J., Xia N.S.;
RT "Colorful mutants of green fluorescent protein from Aequorea
RT macrodactyla.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF435429; AAL33914.1;
DR InterPro; IPR000786; Green_fl_protein.
DR Pfam; PF01353; GFP; 1.
DR ProDom; PD013756; Green_fl_protein; 1.
SQ SEQUENCE 238 AA; 27047 MW; 5F80A18FA1E7C84D CRC64;
Query Match 84.3%; Score 1074; DB 5; Length 238;
Best Local Similarity 81.5%; Pred. No. 6.4e-61;
Matches 194; Conservative 24; Indels 0; Gaps 0;
QY 2 VSKGEELFTGVPLVLELDGVNKHKFSVSGEGDGYATYKGLTKLFCTCTCKLPVWPPTL 61
DB 1 VSKGEELFTGVPLVLELDGVNKHKFSVSGEGDGYATYKGLTKLFCTCTCKLPVWPPTL 60
QY 62 VTTLSGVQCFSPYDPMKHQDFPKSAMPEGYQVQERTIFFKDDGNYKTRAEVKEGDTLV 121
DB 61 VTTLSGVQCFSPYDPMKHQDFPKSAMPEGYQVQERTIFFKDDGNYKTRAEVKEGDTLV 120
QY 122 NRTELKGFDEKNGHLKLEYNFNSHNYIMADKQKNGIKVNFKIRHNIDSGVOLAD 181
DB 121 NRTELKGFDEKNGHLKLEYNFNSHNYIMADKQKNGIKVNFKIRHNIDSGVOLAD 180
QY 182 HYQNTPTIGDGPVLPDNYLSQTASLKDQPKRDNHVLGFTVTAAGITLGMDELK 239
DB 181 HYQNTNPLDGPVLPINHYLSQTASLKDQPKRDNHVLGFTVTAAGITLGMDELK 238
RESULT 12
QY Q8WTC7 PRELIMINARY; PRT; 238 AA.
AC Q8WTC5;
DB DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE The green fluorescent protein.

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GN GFP.
OS Aequorea macrodactyla.
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroids; Leptomedusae;
OC Aequoreidae; Aequorea.
OX NCBI_TaxID=147615;
RN RP
RC STRAIN=GFXM191U;
RA Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.,
RA Li S.J., Xia N.S.;
RT "Colorful mutants of green fluorescent protein from Aequorea
RT macrodactyla.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF435430; AAL33915.1;
DR InterPro; IPR000786; Green_fl_protein.
DR Pfam; PF01353; GFP; 1.
DR ProDom; PD013756; Green_fl_protein; 1.
SQ SEQUENCE 238 AA; 27002 MW; BD5BA298226AC018 CRC64;
Query Match 84.1%; Score 1072; DB 5; Length 238;
Best Local Similarity 81.5%; Pred. No. 9.4e-61;
Matches 194; Conservative 20; Mismatches 24; Indels 0; Gaps 0;
QY 2 VSKGEELFTGVPLVLELDGVNKHKFSVSGEGDGYATYKGLTKLFCTCTCKLPVWPPTL 61
DB 1 VSKGEELFTGVPLVLELDGVNKHKFSVSGEGDGYATYKGLTKLFCTCTCKLPVWPPTL 60
QY 62 VTTLSGVQCFSPYDPMKHQDFPKSAMPEGYQVQERTIFFKDDGNYKTRAEVKEGDTLV 121
DB 61 VTTLSGVQCFSPYDPMKHQDFPKSAMPEGYQVQERTIFFKDDGNYKTRAEVKEGDTLV 120
QY 122 NRTELKGFDEKNGHLKLEYNFNSHNYIMADKQKNGIKVNFKIRHNIDSGVOLAD 181
DB 121 NRTELKGFDEKNGHLKLEYNFNSHNYIMADKQKNGIKVNFKIRHNIDSGVOLAD 180
QY 182 HYQNTPTIGDGPVLPDNYLSQTASLKDQPKRDNHVLGFTVTAAGITLGMDELK 239
DB 181 HYQNTNPLDGPVLPINHYLSQTASLKDQPKRDNHVLGFTVTAAGITLGMDELK 238
RESULT 13
QY Q8WTC5 PRELIMINARY; PRT; 238 AA.
AC Q8WTC5;
DB DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE The green fluorescent protein.
GN GFP.
OC Aequorea macrodactyla.
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroids; Leptomedusae;
OC Aequoreidae; Aequorea.
OX NCBI_TaxID=147615;
RN RP
RC STRAIN=GFXM191U;
RA Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.,
RA Li S.J., Xia N.S.;
RT "Colorful mutants of green fluorescent protein from Aequorea
RT macrodactyla.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF435430; AAL33917.1;
DR InterPro; IPR000786; Green_fl_protein.
DR Pfam; PF01353; GFP; 1.
DR ProDom; PD013756; Green_fl_protein; 1.
SQ SEQUENCE 238 AA; 27018 MW; 75521EA5534E573A CRC64;
Query Match 84.0%; Score 1070; DB 5; Length 238;
Best Local Similarity 82.4%; Pred. No. 1.4e-80;
Matches 196; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 2 VSKGEELFTGVPLVLELDGVNKHKFSVSGEGDGYATYKGLTKLFCTCTCKLPVWPPTL 61
DB 1 VSKGEELFTGVPLVLELDGVNKHKFSVSGEGDGYATYKGLTKLFCTCTCKLPVWPPTL 60

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Db 1 MSKGEELFTQWPIVLVDGDNHGKFSVRGEGDADYKGLKIFCTTGKLPVPMPTL 60
Qy 62 VTLISYGVGCVSRVPOHKHDFKFSAMPEGVQERTIFFKDGNGYKTRAEVFGDTLV 121
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 VTLVGLGLFCFAFYEPKHKNDFFKFSAMPEGVQERTIFFQDDGCKYKTRAEVFGDTLV 120
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 122 NRLEKGIKFDKNGTLGKLEYNVSHNYIMADKQKIKVNFKIRINIEDGSQLAD 181
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 NRLEKGIKFDKNGTLGKLEYNVSHNYIMADKQKIKVNFKIRINIEDGSQLAD 180
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 182 HYQONTPIGDGCPVLLPDNHYLSQTOSALSDKPRKDHVVLGFTVGAAGTIGHDLK 239
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 HYQONTPIGDGCPVLLPDNHYLSQTOSALSDKPRKDHVVLGFTVGAAGTIGHDLK 238

RESULT 14
ID Q95DU7 PRELIMINARY; PRT: 225 AA.
AC Q95DU7
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cyan fluorescent protein (Fragment).
OS Montastraea cavernosa (great star coral).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;
OC Faviina; Faviidae; Montastraea.
OX NCBI_TaxID=63558;
RN [1]
RP SEQUENCE FROM N.A.
RA Falkowski P.G., Sun Y.;
RI Montastraea cavernosa fluorescent protein.*;
RI Submitted (1995) to the EMBL/GenBank/DBJ databases.
DI EMBL:AY056460; A017905
DR InterPro: IPR000786; Green_fl_protein.
DR Pfam: PF01353; GFP.1.
DR ProDom: PD013756; Green_fl_protein.1.
ET NON_TER 225 225
SQ SEQUENCE 225 AA; 25775 MW; 52DE2F716D083524 CRC64;

Query Match 19.8%; Score 252.5; DB 5; Length 225;
Best Local Similarity 31.1%; Pred. No. 3, 8e-13;
Matches 64; Conservative 82; Mismatches 82; Indels 17; Gaps 7;

Qy 12 VVPIVLVDGDNHGKFSVRGEGDADYKGLKIFCTTGKLPVPMPTLVTLISYGV 70
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7 VKIKLMDGLVNGHKFMFTVGGSGSPFEGTHILAKVEGCPLPFAYDILTAPOYGNR 66
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 71 CFSRYPDHKQIDFFKFSAMPEGVQERTIFFKDGNGYKTRAEVFGDTLVNRIELK 130
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 67 VFTKYPDIP--DYFQTFPEGSYMERINAVFQSICTATSDIRMEDCFIYELQPGV 124
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 131 FKEDNTILGHK--LEYNYSNHYIMADKQKIKVNFKIRINIEDGSQLAD----- 183
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 125 FFSGPGVWOKTKLKEPSTEKY-----VRDGLVKGDNVLMALLEGGHY 169
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 184 Q---QNTPTGDCPVLLPDNHYLSQTOSALSKOPNE 214
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 170 RCDFRSTYKAKKRVLPDYHFVDRHRIELSHND 203

Search completed: June 3, 2003, 15:08:36
Job time : 85 secs

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RESULT 15
ID Q963F5 PRELIMINARY; PRT: 225 AA.
AC Q963F5
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Green fluorescent protein.
OS Montastraea cavernosa (great star coral).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;
OC Faviina; Faviidae; Montastraea.
OX NCBI_TaxID=63558;
RN [1]

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